Lost in translation from genes to organisms

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Abstract. Data mining genomes and developmental genetics provides information for building mathematical gene-network models on development. These models can be used to provide in-silico predictions about processes such as developmental expression and regulation of genes. At the higher levels of biological organization, at levels of micro- and macroevolution, models can be used to 'translate' knowledge on development and genes to phenotypes in order to test how development affects evolution of phenotypes. However, several challenges remain. In contrasts to the tools to study genomes, analysis and data mining of three-dimensional phenotype remains cumbersome. Furthermore, understanding the regulatory code, often assumed to link the genetic code and the phenotype, may be not sufficient alone and a higher level 'phenotype code' may be required to disentangle the logic of genetic networks.